

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> METHOD FOR SCREENING CANDIDATE COMPOUNDS FOR ANTITUMOR DRUG

<130> C1-003PCT

<150> JP 1998-233729

<151> 1998-08-20

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 319

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(318)

<223> FLT3/ITD gene (Mt1); partial sequence

<400> 1

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser

1

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10

15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat 96

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp

20

25

30

ctc aaa tgg gag ttt cca aga gaa aat tgc tcc tca gat aat gag tac 144

Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr

35

40

45

ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt 192
 Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 50 55 60

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 240
 Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 65 70 75 80

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 288
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 85 90 95

tca atc cag gtt gcc gtc aaa atg ctg aaa g 319
 Ser Ile Gln Val Ala Val Lys Met Leu Lys
 100 105

<210> 2

<211> 106

<212> PRT

<213> Homo sapiens

<220>

<223> FLT3/ITD (Mt1); partial sequence
 ITD region (42)..(68)

<400> 2

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
 20 25 30

Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr

35

40

45

Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe

50

55

60

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe

65

70

75

80

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val

85

90

95

Ser Ile Gln Val Ala Val Lys Met Leu Lys

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105

<210> 3

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(297)

<223> FLT3/ITD gene (Mt2); partial sequence

<400> 3

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser

1

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10

15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat 96

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp

20

25

30

ctc aaa agc tcc tca gat aat gag tac ttc tac gtt gat ttc aga gaa 144

Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu

35	40	45	
tat gaa tat gat ctc aaa tgg gag ttt cca aga gaa aat tta gag ttt			192
Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe			
50	55	60	
ggg aag gta cta gga tca ggt gct ttt gga aaa gtg atg aac gca aca			240
Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr			
65	70	75	80
gct tat gga att agc aaa aca gga gtc tca atc cag gtt gcc gtc aaa			288
Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys			
85	90	95	
atg ctg aaa g			298
Met Leu Lys			

<210> 4

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<223> FLT3/ITD (Mt2); partial sequence

ITD region (35)..(54)

<400> 4

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
1 5 10 15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
20 25 30

Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu
35 40 45

Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe
 50 55 60

Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr
 65 70 75 80

Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys
 85 90 95

Met Leu Lys

<210> 5

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(270)

<223> FLT3/ITD gene (Mt3); partial sequence

<400> 5

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa atg gga 96
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly
 20 25 30

atg ggg gga gaa tgt aat ccc ggg aga caa gat ctc aaa tgg gag ttt 144
 Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe
 35 40 45

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 192
 Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe

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60

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 240
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val

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75

80

tca atc cag gtt gcc gtc aaa atg ctg aaa g 271
 Ser Ile Gln Val Ala Val Lys Met Leu Lys

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<210> 6

<211> 90

<212> PRT

<213> Homo sapiens

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<223> FLT3/ITD (Mt3); partial sequence
 ITD region (31)..(42)

<400> 6

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser

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Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly

20

25

30

Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe

35

40

45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe

50

55

60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 65 70 75 80

Ser Ile Gln Val Ala Val Lys Met Leu Lys
 85 90

<210> 7

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(270)

<223> FLT3/ITD gene (Mt4); partial sequence

<400> 7

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gat gag tac 96
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr
 20 25 30

ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt 144
 Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 35 40 45

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 192
 Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 50 55 60

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 240
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val

65

70

75

80

tca atc cag gtt gcc gtc aaa atg ctg aaa g

271

Ser Ile Gln Val Ala Val Lys Met Leu Lys

85

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<210> 8

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<223> FLT3/ITD (Mt4); partial sequence

ITD region (30)..(40)

<400> 8

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser

1

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10

15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr

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30

Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe

35

40

45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe

50

55

60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val

65

70

75

80

Ser Ile Gln Val Ala Val Lys Met Leu Lys

85

90

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A primer for
amplifying human FLT3/ITD genes

<400> 9
caacaattgg tgtttgtctc ctctt

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<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A primer for
amplifying human FLT3/ITD genes.

<400> 10
catgatatct cgagccaatc caaag